What is claimed is:

Claims

- 1. A substantially pure human nucleic acid comprising at least 40 nucleotides that hybridizes under high stringency conditions to a sequence found within the nucleic acid of SEQ ID NO:1.
 - 2. The nucleic acid of claim 1, wherein said sequence has a sequence complementary to at least 50% of at least 60 contiguous nucleotides of the nucleic acid encoding the methionine synthase polypeptide, said sequence sufficient to allow nucleic acid hybridization under high stringency conditions.

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- 3. The nucleic acid of claim 1, wherein said nucleic acid comprises a mutation or a polymorphism, wherein said nucleic acid probe detects a mutation or polymorphism selected from the group consisting of D919G, H920D, and ΔIle881.
- 4. The nucleic acid of claim 3, wherein said sequence of said nucleic acid comprises the cobalamin binding domain of the human methionine synthase gene.
- 5. The nucleic acid of claim 2, wherein at least 18 contiguous nucleotides of said sequence are complementary to at least 90% of the corresponding nucleotides of the nucleic acid encoding the methionine synthase polypeptide.
- 6. The nucleic acid of claim 1, wherein said high stringency conditions comprise hybridization in 2X SSC at 40°C.
 - 7. A substantially pure human nucleic acid, wherein the sequence of said nucleic acid is at least 75% identical to the corresponding region of at least 50 contiguous base pairs of the nucleic acid of SEQ ID NO:1.

- 8. A substantially pure human nucleic acid, wherein the sequence of said nucleic acid is at least 35% identical to the corresponding region of at least 50 contiguous base pairs of the nucleic acid of SEQ ID NO:1.
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- 9. A kit for the analysis of a human methionine synthase nucleic acid, said kit comprising a nucleic acid probe useful for detecting in the nucleic acids of a human a mutation or polymorphism in said methionine synthase nucleic acid, wherein said mutation or polymorphism is selected from the group consisting of D919G, H920D, and ΔIle881.
- 10. The kit of claim 9, wherein said probe comprises at least 40 nucleotides that hybridizes at high stringency to a sequence found within the nucleic acid of SEQ ID NO:1.